the nucleotide sequence of the oligonucleotide probe is completely complementary to the template molecule to which it is bound will quenching be removed. A reaction mix can contain two different probe sequences each designed against different alleles that might be present, thus, allowing the detection of both alleles in on reaction.

On page 10, the paragraph at lines 5 and 6 has been replaced with the following:

MC4R1: 5' TGG CAA TAG CCA AGA ACA AG 3' (SEQ ID NO: 5)

MC4R4: 5' CAG GGG ATA GCA ACA GAT GA 3' (SEQ ID NO: 6)

On page 11, the paragraph at lines 27 and 28 has been replaced with the following:

Figures 2 and 3 illustrate the differences between the DNA and amino acid sequences of the human and porcine MC4R gene (SEQ ID NOS: 1-4).

On page 12, the paragraph at lines 20 and 21 has been replaced with the following:

Forward primer: 5'-TTA AGT GGA GGA AGA AGG-3' (SEQ ID NO: 7)

Reverse primer: 5'-CAT TAT GAC AGT TAA GCG G-3' (SEQ ID NO: 8)

In the Claims

Please cancel claims 12, 28 and 31.

Please the following claims:

1. (Thrice Amended)

A method for identifying an animal which possesses a genotype associated with one or more favorable metabolic traits selected from fat content, growth rate, and feed consumption, the method comprising:

obtaining a nucleic acid sample from an animal; and

detecting a polymorphism at position 678 of SEQ ID NO: 1 wherein said polymorphism is associated with one or more of the metabolic traits of fat content, growth rate, and feed consumption.

2. (Thrice Amended)

The method of claim 1 wherein the polymorphism is detected at position 678 of a PCR sequence using a forward primer and a reverse primer.

4. (Thrice Amended)

The method of claim 2 wherein the polymorphism detected at base 678 is a guanine the polymorphism being associated with fat content.

5. (Thrice Amended)

The method of claim 2 wherein the polymorphism for lower feed intake, than animals without the marker, is an adenine at base 678.

6. (Thrice Amended)

The method of claim 2 wherein the polymorphism for faster rate of gain, than animals without the polymorphism, is an adenine at base 678 of a PCR sequence.

20. (Thrice Amended)

A method of identifying an animal which possess a genotype associated with one or more metabolic traits selected from fat content, growth rate, and feed consumption, the method comprising:

obtaining a nucleic acid sample from an animal;

amplifying nucleic acid of said sample with primers SEQ ID NO: 5 and SEQ ID NO: 6.

sequencing the amplified product to reveal a nucleotide substitution within a *Taq I* restriction enzyme recognition site;

digesting the amplified product with *Taq I* to obtain fragments;

separating the fragments obtained from the digestion, and

generating a MC4R gene fragment having one *Taq I* restriction site with primers SEQ ID NO: 9 and SEQ ID NO: 10; and

identifying the presence or absence of a *Taq I* site

wherein the presence of a *Taq I* restriction pattern in said genotype identifies the presence of a polymorphic site in the MC4R gene.

22. (Amended)

The method of claim 20 wherein the restriction pattern generated is identifiable by fragments of 466, 225, and 76 bp which is indicative of an animal having lower backfat, lower daily rate of gain and lower feed intake than an animal without the polymorphism.

29. (Twice Amended)

A method for an indirect selection of a polymorphism in a MC4R gene associated with variation in one or more metabolic traits selected from fat content, growth rate, and feed consumption comprising:

establishing a linkage between the specific alleles of an alternative DNA maker and alleles of the DNA marker known to be associated with a metabolic trait selected from the group consisting of fat content, growth rate, and feed consumption and

selecting for the polymorphism with the alternative DNA marker.

30. (Amended)

The method of claim 29 wherein the linked marker known to be associated with the metabolic trait is selected from the group consisting of S0331, BHT0433, and S0313.

Please add new claims 34-36:

34. (New)

The method of claim 2 wherein the forward primer is SEQ ID NO: 5 and the reverse primer is SEQ ID NO: 6.

35. (New)

The method of claim 2 wherein the forward primer is SEQ ID NO: 7 the reverse primer is SEQ ID NO: 8.

36. (New)

The method of claim 2 wherein the forward primer is SEQ ID NO: 9 and the reverse primer is SEQ ID NO: 10.